



# SEQUENCE LISTING

<110> Nelson B. Freimer  
Hong Chen  
Victor I. Reus  
Susan K. Service  
Lynne Alison McInnes  
Pedro Leon  
Lodewijk Sandkuijl

<120> Method and Compositions for Diagnosing and Treating Chromosome-18p  
Related Disorders

<130> UCAL-154CIP5

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gcatcttagg aatgacagag ttgcgtccct ctctgttgcc aggctggagt tcagtggcat	180
gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctcca cctcagcccc	240
atgaggacct gggactacag gacacagcta aatccctgac acgg atg aaa att aaa	296
Met Lys Ile Lys	

gca gag aaa aac gaa ggt cct tcc aga agc tgg tgg caa ctt cac tgg	344
Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His Trp	
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gga gat att gca aat aac agc ggg aac atg aag ccg cca ctc ttg gtg	392
Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu Val	
25 30 35	
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Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro Thr	
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tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt tct gag	488
Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser Glu	
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gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg act ggt	536
Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr Gly	
70 75 80	
att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa cac acc	584
Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His Thr	
85 90 95 100	
aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag gag gcc	632
Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu Ala	
105 110 115	
ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa gaa agg	680
Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu Arg	
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cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg tct tgc	728
Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys	
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Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser Trp	
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Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu Asp Val	
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Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg Ser Phe	
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Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe Gln Ser	

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cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca gaa tta His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr Glu Leu 360 365 370			1400
gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat ggc cag Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr Gly Gln 375 380 385			1448
att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat ctg gtg Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr Leu Val 390 395 400			1496
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gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt cca agg Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val Pro Arg 425 430 435			1592
att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg aca gac Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met Thr Asp 440 445 450			1640
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 Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys  
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 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu  
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 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp  
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 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln  
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 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr  
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 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu  
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 Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser  
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 Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys  
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 Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly  
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Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
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 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr  
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 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
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gttcatagct cactgaagcc tcaaattcct gggttcaagt gaccctccta cctcagcccc	240
atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc	288
Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu	
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Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Ser Ala	
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ccc act tgg aag gac aaa agt gct atc agt gaa aac ctg aag agt ttt	384
Pro Thr Trp Lys Asp Lys Ser Ala Ile Ser Glu Asn Leu Lys Ser Phe	
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tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg	432
Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu	
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act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gca	480
Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Ala	
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Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val	
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cca agg att gaa cac acc aat cta atg agc acc ctg aag aaa tgc aga	576
Pro Arg Ile Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg	
100 105 110	
gaa gaa aag cag gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat	624

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Leu	Glu	Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	
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ggt	gaa	tgc	agg	tct	tgc	ctg	gaa	aat	aac	tgc	atg	aga	att	tat	aca	720
Gly	Glu	Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	
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Thr	Cys	Gln	Pro	Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	
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Phe	Arg	Lys	Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	
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aaa	gat	ctc	ccc	atc	agt	gaa	aag	ctc	att	gag	gaa	gat	gca	caa	ttg	864
Lys	Asp	Leu	Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	
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acc	caa	atg	gag	gat	gtg	ttc	agc	cag	ttg	act	gtg	gat	gtg	aat	tct	912
Thr	Gln	Met	Glu	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	
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cct	tac	ttt	ttt	cca	gct	ttc	tct	aaa	gag	ccg	atg	aca	aaa	gca	gat	1056
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Leu	Glu	Gln	Cys	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	
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Phe	Ser	Val	Ser	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	
	290					295				300						
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Leu	Lys	Ala	Ile	Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	
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ggg	gaa	ctt	gac	cag	aat	ttg	tca	aga	tgt	ttc	aaa	ttt	cat	gaa	aaa	1296
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370	375	380	
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gac acc gcc tat ctg gtg gag aag atg aga ggg caa ttt ggc tgg gtg			1488
Asp Thr Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val			
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Ser Glu Leu His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met			
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Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro			
435	440	445	
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465	470	475	
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Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu			
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115 120 125			
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130 135 140			

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Phe	Arg	Lys	Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu
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Lys	Asp	Leu	Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu
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Thr	Gln	Met	Glu	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser
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Leu	Glu	Gln	Cys	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn
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Gly	Gly	Leu	Ile	Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys
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Gly	Glu	Leu	Asp	Gln	Asn	Leu	Ser	Arg	Cys	Phe	Lys	Phe	His	Glu	Lys
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Asn	Gln	Gln	Tyr	Gly	Gln	Ile	Leu	Gln	Met	Thr	Arg	Lys	His	Leu	Glu
385					390					395					400
Asp	Thr	Ala	Tyr	Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val
			405						410					415	
Ser	Glu	Leu	His	Glu	Gly	Asn	Ile	Ser	Lys	Gln	Asp	Glu	Thr	Met	Met
			420					425					430		
Thr	Asp	Leu	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Leu	Lys	Ile	Pro
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Leu	Glu	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Phe	Ile	Gly	Tyr	Val	Val	Ala
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 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
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cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
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Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys	
270 275 280	
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Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala	
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Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala	
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His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser	
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 Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys  
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 His Leu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser  
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 115 120 125  
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 420 425 430  
 Thr Leu Ser Ser Pro Leu Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile  
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 Thr Trp  
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 actgcaagga ttaacagtga gaac atg aag ctg cca ctt ttg atg ttt ccc 171  
 Met Lys Leu Pro Leu Leu Met Phe Pro  
 1 5  
  
 gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
 10 15 20 25  
  
 gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
 Asp Lys Thr Ala Ile Ser Glu Asn Ala Asn Ser Phe Ser Glu Ala Gly  
 30 35 40  
  
 gag ata gac gta gat gga gag gtg aag ata gct ttg att ggc att aaa 315  
 Glu Ile Asp Val Asp Gly Glu Val Lys Ile Ala Leu Ile Gly Ile Lys  
 45 50 55  
  
 cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu  
 60 65 70  
  
 atg aaa acc ttg aag aag tgc aaa gaa gaa aag cag gag gcc ctg aaa 411  
 Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys  
 75 80 85  
  
 ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc 459  
 Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys  
 90 95 100 105  
  
 cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa 507  
 Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu  
 110 115 120  
  
 agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct 555  
 Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser  
 125 130 135

gtg aaa aat atg gaa aat gac aga agt ggc cct gtc agc aaa ggg gtc	603
Val Lys Asn Met Glu Asn Asp Arg Ser Gly Pro Val Ser Lys Gly Val	
140 145 150	
act gag gaa gat gcg cag gtg tca cac ata gag cat gtg ttc agc cag	651
Thr Glu Glu Asp Ala Gln Val Ser His Ile Glu His Val Phe Ser Gln	
155 160 165	
ctg agc gca gat gtg aca tct ctc ttc aac aga agc ctt tac gtc ttc	699
Leu Ser Ala Asp Val Thr Ser Leu Phe Asn Arg Ser Leu Tyr Val Phe	
170 175 180 185	
aaa cag ctg cgg cga gaa ttt gac cag gct ttt cag tca tat ttc aca	747
Lys Gln Leu Arg Arg Glu Phe Asp Gln Ala Phe Gln Ser Tyr Phe Thr	
190 195 200	
tcg ggg act gac gtt aca gag cct ttc ttt ttt cca tct ttg tcc aag	795
Ser Gly Thr Asp Val Thr Glu Pro Phe Phe Phe Pro Ser Leu Ser Lys	
205 210 215	
gag cca gcc tac aga gca gat gct gag cca agc tgg gcc att ccc aat	843
Glu Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala Ile Pro Asn	
220 225 230	
gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt tat caa agt gtc	891
Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr Gln Ser Val	
235 240 245	
agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag gac cct cca aaa	939
Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys	
250 255 260 265	
caa gac aaa gac tcc aac cag gga ggc ccg att tca aag ata cta cct	987
Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys Ile Leu Pro	
270 275 280	
gag caa gac aga ggc tca gat ggg aaa ctt ggc cag aat ttg tct gat	1035
Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp	
285 290 295	
tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag gat tat cta tct	1083
Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser	
300 305 310	
gat gac tgc cct aat gtg cct gaa cta tac aga gaa ctc aat gag gcc	1131
Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala	
315 320 325	
ctc cga ctg gtc agt aga tcc aat cag caa tac gac cag gtg gtg cag	1179
Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp Gln Val Val Gln	
330 335 340 345	
atg acc cag tat cac ctg gaa gac acc acg ctt ctg atg gag aag atg	1227
Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu Met Glu Lys Met	
350 355 360	
aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac cag tcc cca gga	1275
Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr Gln Ser Pro Gly	
365 370 375	

gct gag gac atc ttt aat cca gtg aaa gta atg gta gcc cta agt gct	1323
Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala	
380 385 390	
cat gaa gga aat tct tct gat caa gat gac aca gtg gtt cct tca agc	1371
His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser	
395 400 405	
ctc ctg cct tcc tct aac ttc aca ctc agc agc cct ctt gaa aag agt	1419
Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro Leu Glu Lys Ser	
410 415 420 425	
gct ggc aac gct aac ttc att gat cac gtg gta gag aag gtt ctt cag	1467
Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu Lys Val Leu Gln	
430 435 440	
cac ttt aag gag cac ttt aaa act tgg taagaagatt tagtccatcc	1514
His Phe Lys Glu His Phe Lys Thr Trp	
445 450	
tataatcagc aagaattaca ccttcggcca agacctgaga attctgaaaa tacaaagcag	1574
gctaacacaa tgaacacagc tgcattgaaag ttaggtatat attaggaagc actattgggt	1634
tactttgttg aatggaagtt taatagctat tcaaattgag ttaatatataa aattttcttc	1694
taaaaagtaa aatgtacata tgtagaatat gatgcattag ttctttgtat actaaataaa	1754
tactgagtcc cct	1767
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Asn Ala Asn Ser Phe Ser Glu Ala Gly Glu Ile Asp Val Asp Gly Glu	
35 40 45	
Val Lys Ile Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu	
50 55 60	
Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys	
65 70 75 80	
Lys Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu Val His Glu	
85 90 95	
His Leu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser	
100 105 110	
Trp Asp Glu Cys Arg Ala Cys Leu Glu Ser Asn Cys Met Arg Phe Asp	
115 120 125	
Thr Thr Cys Gln Pro Ala Trp Ser Ser Val Lys Asn Met Glu Asn Asp	
130 135 140	
Arg Ser Gly Pro Val Ser Lys Gly Val Thr Glu Glu Asp Ala Gln Val	
145 150 155 160	
Ser His Ile Glu His Val Phe Ser Gln Leu Ser Ala Asp Val Thr Ser	
165 170 175	
Leu Phe Asn Arg Ser Leu Tyr Val Phe Lys Gln Leu Arg Arg Glu Phe	
180 185 190	
Asp Gln Ala Phe Gln Ser Tyr Phe Thr Ser Gly Thr Asp Val Thr Glu	
195 200 205	
Pro Phe Phe Phe Pro Ser Leu Ser Lys Glu Pro Ala Tyr Arg Ala Asp	



[illegible]

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cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu 110 115 120			507
agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser 125 130 135			555
gtg aaa aat atg gag cca gcc tac aga gca gat gct gag cca agc tgg Val Lys Asn Met Glu Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp 140 145 150			603
gcc att ccc aat gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt Ala Ile Pro Asn Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val 155 160 165			651
tat caa agt gtc agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag Tyr Gln Ser Val Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu 170 175 180 185			699
gac cct cca aaa caa gac aaa gac tcc aac cag gga ggc ccg att tca Asp Pro Pro Lys Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser 190 195 200			747
aag ata cta cct gag caa gac aga ggc tca gat ggg aaa ctt ggc cag Lys Ile Leu Pro Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln 205 210 215			795
aat ttg tct gat tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag Asn Leu Ser Asp Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln 220 225 230			843
gat tat cta tct gat gac tgc cct aat gtg cct gaa cta tac aga gaa Asp Tyr Leu Ser Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu 235 240 245			891
ctc aat gag gcc ctc cga ctg gtc agt aga tcc aat cag caa tac gac Leu Asn Glu Ala Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp 250 255 260 265			939
cag gtg gtg cag atg acc cag tat cac ctg gaa gac acc acg ctt ctg Gln Val Val Gln Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu 270 275 280			987
atg gag aag atg aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac Met Glu Lys Met Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr 285 290 295			1035
cag tcc cca gga gct gag gac atc ttt aat cca gtg aaa gta atg gta Gln Ser Pro Gly Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val 300 305 310			1083

gcc cta agt gct cat gaa gga aat tct tct gat caa gat gac aca gtg	1131
Ala Leu Ser Ala His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val	
315 320 325	
gtt cct tca agc ctc ctg cct tcc tct aac ttc aca ctc agc agc cct	1179
Val Pro Ser Ser Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro	
330 335 340 345	
ctt gaa aag agt gct ggc aac gct aac ttc att gat cac gtg gta gag	1227
Leu Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu	
350 355 360	
aag gtt ctt cag cac ttt aag gag cac ttt aaa act tgg taagaagatt	1276
Lys Val Leu Gln His Phe Lys Glu His Phe Lys Thr Trp	
365 370	
tagtccatcc tataatcagc aagaattaca ccttcggcca agacctgaga attctgaaaa	1336
tacaaagcag gctaacacaa tgaacacagc tgcataaag ttaggtatat attaggaagc	1396
actattgggtt tactttgttg aatggaagtt taatagctat tcaaattgag ttaatataaa	1456
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actaaataaa tactgagtcc cct	1539

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 <212> PRT  
 <213> Cavia sp.

<400> 43

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Asn Ala Asn Ser Phe Ser Glu Ala Gly Glu Ile Asp Val Asp Gly Glu	
35 40 45	
Val Lys Ile Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu	
50 55 60	
Arg Arg Glu Glu Glu His Ser Lys Leu Met Lys Thr Leu Lys Lys Cys	
65 70 75 80	
Lys Glu Glu Lys Gln Glu Ala Leu Lys Leu Met Asn Glu Val His Glu	
85 90 95	
His Leu Glu Glu Glu Ser Leu Cys Gln Val Ser Leu Ala Asp Ser	
100 105 110	
Trp Asp Glu Cys Arg Ala Cys Leu Glu Ser Asn Cys Met Arg Phe Asp	
115 120 125	
Thr Thr Cys Gln Pro Ala Trp Ser Ser Val Lys Asn Met Glu Pro Ala	
130 135 140	
Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala Ile Pro Asn Val Phe Gln	
145 150 155 160	
Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr Gln Ser Val Ser Glu Lys	
165 170 175	
Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp Pro Pro Lys Gln Asp Lys	
180 185 190	
Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys Ile Leu Pro Glu Gln Asp	
195 200 205	
Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp Cys Val Asn	
210 215 220	
Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser Asp Asp Cys	
225 230 235 240	
Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu Asn Glu Ala Leu Arg Leu	

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			260					265					270				
Tyr	His	Leu	Glu	Asp	Thr	Thr	Leu	Leu	Met	Glu	Lys	Met	Arg	Glu	Gln		
		275					280					285					
Phe	Gly	Trp	Val	Ser	Glu	Leu	Ala	Tyr	Gln	Ser	Pro	Gly	Ala	Glu	Asp		
	290					295					300						
Ile	Phe	Asn	Pro	Val	Lys	Val	Met	Val	Ala	Leu	Ser	Ala	His	Glu	Gly		
305					310					315					320		
Asn	Ser	Ser	Asp	Gln	Asp	Asp	Thr	Val	Val	Pro	Ser	Ser	Leu	Leu	Pro		
			325						330					335			
Ser	Ser	Asn	Phe	Thr	Leu	Ser	Ser	Pro	Leu	Glu	Lys	Ser	Ala	Gly	Asn		
			340					345					350				
Ala	Asn	Phe	Ile	Asp	His	Val	Val	Glu	Lys	Val	Leu	Gln	His	Phe	Lys		
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Glu	His	Phe	Lys	Thr	Trp												
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 <213> Cavia sp.

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 actgcaagga ttaacagtga gaac atg aag ctg cca ctt ttg atg ttt ccc 171  
 Met Lys Leu Pro Leu Leu Met Phe Pro  
 1 5

gtg tgt ctg cta tgg ttg aaa gac tgt cat tgt gca cct act tgg aag 219  
 Val Cys Leu Leu Trp Leu Lys Asp Cys His Cys Ala Pro Thr Trp Lys  
 10 15 20 25

gac aaa act gcc atc agt gaa aac gcg aac agt ttt tct gag gct ggg 267  
 Asp Lys Thr Ala Ile Ser Glu Asn Ala Asn Ser Phe Ser Glu Ala Gly  
 30 35 40

gag ata gac gta gat gga gag gtg aag ata gct ttg att ggc att aaa 315  
 Glu Ile Asp Val Asp Gly Glu Val Lys Ile Ala Leu Ile Gly Ile Lys  
 45 50 55

cag atg aaa atc atg atg gaa agg aga gag gaa gaa cac agc aaa cta 363  
 Gln Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ser Lys Leu  
 60 65 70

atg aaa acc ttg aag aag tgc aaa gaa gaa aag cag gag gcc ctg aaa 411  
 Met Lys Thr Leu Lys Lys Cys Lys Glu Glu Lys Gln Glu Ala Leu Lys  
 75 80 85

ctt atg aat gaa gtt cat gaa cac ctg gag gag gaa gaa agc tta tgc 459  
 Leu Met Asn Glu Val His Glu His Leu Glu Glu Glu Glu Ser Leu Cys  
 90 95 100 105

cag gtt tct ctg gca gat tcc tgg gat gaa tgc agg gct tgc ctg gaa 507  
 Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu Glu  
 110 115 120

agt aac tgc atg agg ttt gat acc acc tgc caa cct gca tgg tcc tct	555
Ser Asn Cys Met Arg Phe Asp Thr Thr Cys Gln Pro Ala Trp Ser Ser	
125 130 135	
gtg aaa aat atg cca gcc tac aga gca gat gct gag cca agc tgg gcc	603
Val Lys Asn Met Pro Ala Tyr Arg Ala Asp Ala Glu Pro Ser Trp Ala	
140 145 150	
att ccc aat gtc ttc cag ctg ctc tgc aac ttg agt ttc tca gtt tat	651
Ile Pro Asn Val Phe Gln Leu Leu Cys Asn Leu Ser Phe Ser Val Tyr	
155 160 165	
caa agt gtc agt gaa aaa ctc atc aca acc ctg cgt gcc aca gag gac	699
Gln Ser Val Ser Glu Lys Leu Ile Thr Thr Leu Arg Ala Thr Glu Asp	
170 175 180 185	
cct cca aaa caa gac aaa gac tcc aac cag gga ggc ccg att tca aag	747
Pro Pro Lys Gln Asp Lys Asp Ser Asn Gln Gly Gly Pro Ile Ser Lys	
190 195 200	
ata cta cct gag caa gac aga ggc tca gat ggg aaa ctt ggc cag aat	795
Ile Leu Pro Glu Gln Asp Arg Gly Ser Asp Gly Lys Leu Gly Gln Asn	
205 210 215	
ttg tct gat tgc gtt aat ttt cgc aag aga tgc cag aaa tgc cag gat	843
Leu Ser Asp Cys Val Asn Phe Arg Lys Arg Cys Gln Lys Cys Gln Asp	
220 225 230	
tat cta tct gat gac tgc cct aat gtg cct gaa cta tac aga gaa ctc	891
Tyr Leu Ser Asp Asp Cys Pro Asn Val Pro Glu Leu Tyr Arg Glu Leu	
235 240 245	
aat gag gcc ctc cga ctg gtc agt aga tcc aat cag caa tac gac cag	939
Asn Glu Ala Leu Arg Leu Val Ser Arg Ser Asn Gln Gln Tyr Asp Gln	
250 255 260 265	
gtg gtg cag atg acc cag tat cac ctg gaa gac acc acg ctt ctg atg	987
Val Val Gln Met Thr Gln Tyr His Leu Glu Asp Thr Thr Leu Leu Met	
270 275 280	
gag aag atg aga gag cag ttt ggc tgg gtt tct gaa ctg gca tac cag	1035
Glu Lys Met Arg Glu Gln Phe Gly Trp Val Ser Glu Leu Ala Tyr Gln	
285 290 295	
tcc cca gga gct gag gac atc ttt aat cca gtg aaa gta atg gta gcc	1083
Ser Pro Gly Ala Glu Asp Ile Phe Asn Pro Val Lys Val Met Val Ala	
300 305 310	
cta agt gct cat gaa gga aat tct tct gat caa gat gac aca gtg gtt	1131
Leu Ser Ala His Glu Gly Asn Ser Ser Asp Gln Asp Asp Thr Val Val	
315 320 325	
cct tca agc ctc ctg cct tcc tct aac ttc aca ctc agc agc cct ctt	1179
Pro Ser Ser Leu Leu Pro Ser Ser Asn Phe Thr Leu Ser Ser Pro Leu	
330 335 340 345	
gaa aag agt gct ggc aac gct aac ttc att gat cac gtg gta gag aag	1227
Glu Lys Ser Ala Gly Asn Ala Asn Phe Ile Asp His Val Val Glu Lys	
350 355 360	
gtt ctt cag cac ttt aag gag cac ttt aaa act tgg taagaagatt	1273
Val Leu Gln His Phe Lys Glu His Phe Lys Thr Trp	

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actattgggt	tactttgttg	aatggaagtt	taatagctat	tcaaattgag	ttaatataaa	1453
aattttcttc	taaaaagtaa	aatgtacata	tgtagaatat	gatgcattag	ttctttgtat	1513
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&lt;211&gt; 373

&lt;212&gt; PRT

<213> *Cavia* sp.

&lt;400&gt; 45

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			20					25					30			
Asn	Ala	Asn	Ser	Phe	Ser	Glu	Ala	Gly	Glu	Ile	Asp	Val	Asp	Gly	Glu	
			35				40					45				
Val	Lys	Ile	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	
	50				55					60						
Arg	Arg	Glu	Glu	Glu	His	Ser	Lys	Leu	Met	Lys	Thr	Leu	Lys	Lys	Cys	
65					70				75						80	
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Leu	Lys	Leu	Met	Asn	Glu	Val	His	Glu	
			85					90					95			
His	Leu	Glu	Glu	Glu	Glu	Ser	Leu	Cys	Gln	Val	Ser	Leu	Ala	Asp	Ser	
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Trp	Asp	Glu	Cys	Arg	Ala	Cys	Leu	Glu	Ser	Asn	Cys	Met	Arg	Phe	Asp	
	115						120					125				
Thr	Thr	Cys	Gln	Pro	Ala	Trp	Ser	Ser	Val	Lys	Asn	Met	Pro	Ala	Tyr	
	130					135					140					
Arg	Ala	Asp	Ala	Glu	Pro	Ser	Trp	Ala	Ile	Pro	Asn	Val	Phe	Gln	Leu	
145					150				155						160	
Leu	Cys	Asn	Leu	Ser	Phe	Ser	Val	Tyr	Gln	Ser	Val	Ser	Glu	Lys	Leu	
			165				170						175			
Ile	Thr	Thr	Leu	Arg	Ala	Thr	Glu	Asp	Pro	Pro	Lys	Gln	Asp	Lys	Asp	
			180				185					190				
Ser	Asn	Gln	Gly	Gly	Pro	Ile	Ser	Lys	Ile	Leu	Pro	Glu	Gln	Asp	Arg	
	195				200						205					
Gly	Ser	Asp	Gly	Lys	Leu	Gly	Gln	Asn	Leu	Ser	Asp	Cys	Val	Asn	Phe	
	210				215					220						
Arg	Lys	Arg	Cys	Gln	Lys	Cys	Gln	Asp	Tyr	Leu	Ser	Asp	Asp	Cys	Pro	
225				230					235						240	
Asn	Val	Pro	Glu	Leu	Tyr	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Arg	Leu	Val	
			245				250					255				
Ser	Arg	Ser	Asn	Gln	Gln	Tyr	Asp	Gln	Val	Val	Gln	Met	Thr	Gln	Tyr	
			260				265					270				
His	Leu	Glu	Asp	Thr	Thr	Leu	Leu	Met	Glu	Lys	Met	Arg	Glu	Gln	Phe	
	275					280					285					
Gly	Trp	Val	Ser	Glu	Leu	Ala	Tyr	Gln	Ser	Pro	Gly	Ala	Glu	Asp	Ile	
	290				295					300						
Phe	Asn	Pro	Val	Lys	Val	Met	Val	Ala	Leu	Ser	Ala	His	Glu	Gly	Asn	
305				310					315						320	
Ser	Ser	Asp	Gln	Asp	Asp	Thr	Val	Val	Pro	Ser	Ser	Leu	Leu	Pro	Ser	
			325				330					335				
Ser	Asn	Phe	Thr	Leu	Ser	Ser	Pro	Leu	Glu	Lys	Ser	Ala	Gly	Asn	Ala	
			340				345					350				
Asn	Phe	Ile	Asp	His	Val	Val	Glu	Lys	Val	Leu	Gln	His	Phe	Lys	Glu	
	355						360					365				

<210> 46  
 <211> 2464  
 <212> DNA  
 <213> Bos sp.

<400> 46  
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Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	Lys	Asp	Leu		
			130			135					140						
Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	Thr	Gln	Met		
145				150					155					160			
Glu	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	Leu	Phe	Asn		
			165					170						175			
Arg	Ser	Phe	Asn	Val	Phe	Arg	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln	Thr		
			180					185					190				
Phe	Gln	Ser	His	Phe	Ile	Ser	Asp	Thr	Asp	Leu	Thr	Glu	Pro	Tyr	Phe		
			195			200						205					
Phe	Pro	Ala	Phe	Ser	Lys	Glu	Pro	Met	Thr	Lys	Ala	Asp	Leu	Glu	Gln		

210	215	220
Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val		
225	230	235
Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala		240
	245	250
Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu		255
	260	265
Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu		270
	275	280
Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys		285
	290	295
Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His		300
	305	310
Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln		315
	325	330
Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala		335
	340	345
Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu		350
	355	360
Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val		365
	370	375
Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met		380
	385	390
Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile		395
	405	410
Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val		415
	420	425
Ala Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp		430
	435	440
		445

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<220>  
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44

<210> 53  
 <211> 69  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 53  
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 ttaaaatgc

60  
 69

<210> 54  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 54

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<210> 55  
<211> 41  
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<220>  
<223> Primer

<400> 55  
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<210> 56  
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<220>  
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<400> 56  
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<210> 57  
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<220>  
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<400> 57  
tttttctctc gagacccatga ggacctggga ctacagtaac 40

<210> 58  
<211> 37  
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<220>  
<223> Primer

<400> 58  
tttttctgaa ttcacccatga agccgccact cttggtg 37

<210> 59  
<211> 60  
<212> DNA  
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<220>  
<223> Primer

<400> 59  
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<210> 60  
<211> 36  
<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 60

tttttctctc gaggactaca ggacacagct aaatcc

36

<210> 61

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 61

tttttgatc cttatcacca ggttttaaaa tgttccttaa aatgc

45

<210> 62

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 62

tttttctgaa ttcacccatga agccgccact cttggtg

37

<210> 63

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 63

tttttctctc gagacccatga ggacctggga ctacagtaac

40

<210> 64

<211> 466

<212> PRT

<213> Homo sapiens

<400> 64

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			20					25					30		
Asn	Leu	Lys	Ser	Phe	Ser	Glu	Val	Gly	Glu	Ile	Asp	Ala	Asp	Glu	Glu
			35				40					45			
Val	Lys	Lys	Ala	Leu	Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
			50			55				60					
Arg	Lys	Glu	Lys	Glu	His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys
65					70				75					80	
Arg	Glu	Glu	Lys	Gln	Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu
				85				90						95	
His	Leu	Glu	Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser
			100					105						110	
Trp	Gly	Glu	Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr

	115		120		125
Thr	Thr Cys Gln Pro Ser	Trp Ser Ser Val Lys	Asn Lys Ile Glu Arg		
	130	135	140		
Phe	Phe Arg Lys Ile Tyr	Gln Phe Leu Phe Pro	Phe His Glu Asp Asn		
145		150	155		160
Glu	Lys Asp Leu Pro Ile	Ser Glu Lys Leu Ile	Glu Glu Asp Ala Gln		
	165	170	175		
Leu	Thr Gln Met Glu Asp	Val Phe Ser Gln Leu Thr	Val Asp Val Asn		
	180	185	190		
Ser	Leu Phe Asn Arg Ser	Phe Asn Val Phe Arg	Gln Met Gln Gln Glu		
	195	200	205		
Phe	Asp Gln Thr Phe Gln	Ser His Phe Ile Ser	Asp Thr Asp Leu Thr		
	210	215	220		
Glu	Pro Tyr Phe Phe Pro	Ala Phe Ser Lys Glu	Pro Met Thr Lys Ala		
225		230	235		240
Asp	Leu Glu Gln Cys Trp	Asp Ile Pro Asn Phe	Phe Gln Leu Phe Cys		
	245	250	255		
Asn	Phe Ser Val Ser Ile	Tyr Glu Ser Val Ser	Glu Thr Ile Thr Lys		
	260	265	270		
Met	Leu Lys Ala Ile Glu	Asp Leu Pro Lys Gln	Asp Lys Ala Pro Asp		
	275	280	285		
His	Gly Gly Leu Ile Ser	Lys Met Leu Pro Gly	Gln Asp Arg Gly Leu		
	290	295	300		
Cys	Gly Glu Leu Asp Gln	Asn Leu Ser Arg Cys	Phe Lys Phe His Glu		
305		310	315		320
Lys	Cys Gln Lys Cys Gln	Ala His Leu Ser Glu	Asp Cys Pro Asp Val		
	325	330	335		
Pro	Ala Leu His Thr Glu	Leu Asp Glu Ala Ile	Arg Leu Val Asn Val		
	340	345	350		
Ser	Asn Gln Gln Tyr Gly	Gln Ile Leu Gln Met	Thr Arg Lys His Leu		
	355	360	365		
Glu	Asp Thr Ala Tyr Leu	Val Glu Lys Met Arg	Gly Gln Phe Gly Trp		
	370	375	380		
Val	Ser Glu Leu Ala Asn	Gln Ala Pro Glu Thr	Glu Ile Ile Phe Asn		
385		390	395		400
Ser	Ile Gln Val Val Pro	Arg Ile His Glu Gly	Asn Ile Ser Lys Gln		
	405	410	415		
Asp	Glu Thr Met Met Thr	Asp Leu Ser Ile Leu	Pro Ser Ser Asn Phe		
	420	425	430		
Thr	Leu Lys Ile Pro Leu	Glu Glu Ser Ala Glu	Ser Ser Asn Phe Ile		
	435	440	445		
Gly	Tyr Val Val Ala Lys	Ala Leu Gln His Phe	Lys Glu His Phe Lys		
	450	455	460		
Thr	Trp				
465					

<210> 65  
 <211> 1607  
 <212> DNA  
 <213> H. sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(1607)  
 <223> N = A,T, C, or G

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 tgtgccctcg gctgacttcc agccggtggc acagacgcct ccaggggggca gcactcaagc 120  
 gcatcttagg aatgacagag ttgcgtccct ctctgttgcc aggctggagt tcagtggcat 180  
 gttcttagct cactgaagcc tcaaattcct gggttcaagt gaccctccca cctcagcccc 240



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atgaggacct gggactacag gacacagcta aatccctgac acggatgaaa attaaagcag 300
agaaaaacga aggtccttcc agaagctggt ggcaacttca ctggggagat attgcaaata 360
acagcgggaa catgaagccg ccactcttgg tgtttattgt gtgtctgctg tggttgaaag 420
acagtcactg cgcacccact tgggaaggaca aaactgctat cagtgaaaac ctgaagagtt 480
tttctgaggt gggggagata gatgcagatg aagaggtgaa gaaggctttg actggtatta 540
agcaaatgaa aatcatgatg gaaagaaaag agaaggaaca caccaatcta atgagcacc 600
tgaagaaatg cagagaagaa aagcaggagg ccctgaaact tctgaatgaa gttcaagaac 660
atctggagga agaagaaagg ctatgccggg agtctttggc agattcctgg ggtgaatgca 720
ggtcttgctt ggaaaataac tgcattgagaa ttatataaac ctgccaacct agctggtcct 780
ctgtgaaaaa taagctcctg accacggagg cctgatttca aagatgttac ntgggcagga 840
cagaggactg tgtggggaac ttgaccagaa tttgtcaaga tgtttcaaatt ttcattgaaa 900
atgccaaaaa tgtcaggctc acctatctga agactgtcct gatgtacctg ctctgcacac 960
agaattagac gaggcgatca gggttggtcaa tgtatccaat cagcagtatg gccagattct 1020
ccagatgacc cgaagcactt tggaggacac cgcctatctg gtggagaaga tgagagggca 1080
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aaggattcat gaaggaaata ttccaaaca agatgaaaca atgatgacag acttaagcat 1200
tctgccttcc tctaatttca cactcaagat ccctcttgaa gaaagtgtct agagttctaa 1260
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gtaagaagat ctaatgcac ctatatccag taagtagaat tatctcttca tctgggacct 1380
ggaaatcctg aaataaaaaa ggataatgca ataaacacag ttgcaggaaa gtatgttagc 1440
tatatactat gaagtactct tagtttactt atgttgaatg gcttagctat taatactcaa 1500
attgagttaa aatgaaaatt cctccttaaa aaatcaaacg taatatgtat tacatttcat 1560
ggtacattag tagttctttg tatattgaat aaatactaaa tcaccta 1607

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<210> 66  
 <211> 521  
 <212> PRT  
 <213> Homo sapiens

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<400> 66
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Ala Asp Thr Leu Cys Pro Arg Leu Thr Ser Ser Arg Trp His Arg Arg
20          25          30
Leu Gln Gly Ala Ala Leu Lys Arg Ile Leu Gly Met Thr Glu Leu Arg
35          40          45
Pro Ser Leu Leu Pro Gly Trp Ser Ser Val Ala Cys Ser Leu Thr Glu
50          55          60
Ala Ser Asn Ser Trp Val Gln Val Thr Leu Pro Pro Gln Pro His Glu
65          70          75          80
Asp Leu Gly Leu Gln Asp Thr Ala Lys Ser Leu Thr Arg Met Lys Ile
85          90          95
Lys Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp Gln Leu His
100         105         110
Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro Pro Leu Leu
115         120         125
Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala Pro
130         135         140
Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe Ser
145         150         155         160
Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu Thr
165         170         175
Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu His
180         185         190
Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln Glu
195         200         205
Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu Glu Glu
210         215         220
Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser
225         230         235         240
Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro Ser
245         250         255

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Trp	Ser	Ser	Val	Lys	Asn	Lys	Leu	Leu	Thr	Thr	Glu	Ala	Phe	Gln	Arg		
			260					265					270				
Cys	Tyr	Leu	Gly	Arg	Thr	Glu	Asp	Cys	Val	Gly	Asn	Leu	Thr	Arg	Ile		
		275					280					285					
Cys	Gln	Asp	Val	Ser	Asn	Phe	Met	Lys	Asn	Ala	Lys	Asn	Val	Arg	Leu		
	290					295					300						
Thr	Tyr	Leu	Lys	Thr	Val	Leu	Met	Tyr	Leu	Leu	Cys	Thr	Gln	Asn	Thr		
305					310					315					320		
Arg	Arg	Ser	Gly	Trp	Ser	Met	Tyr	Pro	Ile	Ser	Ser	Met	Ala	Arg	Phe		
			325						330					335			
Ser	Arg	Pro	Gly	Ser	Thr	Trp	Arg	Thr	Pro	Pro	Ile	Trp	Trp	Arg	Arg		
		340						345					350				
Glu	Gly	Asn	Leu	Ala	Gly	Cys	Leu	Asn	Trp	Gln	Thr	Arg	Pro	Gln	Lys		
		355					360					365					
Gln	Arg	Ser	Ser	Leu	Ile	Gln	Tyr	Arg	Phe	Gln	Gly	Phe	Met	Lys	Glu		
	370					375					380						
Ile	Phe	Pro	Asn	Lys	Met	Lys	Gln	Gln	Thr	Ala	Phe	Cys	Leu	Pro	Leu		
385					390					395					400		
Ile	Ser	His	Ser	Arg	Ser	Leu	Leu	Lys	Lys	Val	Leu	Arg	Val	Leu	Thr		
			405						410					415			
Ser	Leu	Ala	Thr	Trp	Gln	Lys	Leu	Tyr	Ser	Ile	Leu	Arg	Asn	Ile	Leu		
		420						425					430				
Lys	Pro	Gly	Lys	Lys	Ile	Cys	Ile	Leu	Tyr	Pro	Val	Ser	Arg	Ile	Ile		
	435					440						445					
Ser	Ser	Ser	Gly	Thr	Trp	Lys	Ser	Asn	Lys	Lys	Gly	Cys	Asn	Lys	His		
	450					455					460						
Ser	Cys	Arg	Lys	Val	Cys	Leu	Tyr	Thr	Met	Lys	Tyr	Ser	Phe	Thr	Tyr		
465					470					475					480		
Val	Glu	Trp	Leu	Ser	Tyr	Tyr	Ser	Asn	Val	Lys	Met	Lys	Ile	Pro	Pro		
			485						490					495			
Lys	Ile	Lys	Arg	Asn	Met	Tyr	Tyr	Ile	Ser	Trp	Tyr	Ile	Ser	Ser	Ser		
		500						505					510				
Leu	Tyr	Ile	Glu	Ile	Leu	Asn	His	Leu									
	515						520										

<210> 67  
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 <212> DNA  
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<220>  
 <223> Primer

<400> 67  
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20

<210> 68  
 <211> 20  
 <212> DNA  
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<220>  
 <223> Primer

<400> 68  
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20

<210> 69  
 <211> 26  
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<220>  
 <223> Primer  
  
 <400> 69  
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 <210> 70  
 <211> 27  
 <212> DNA  
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 <223> Primer  
  
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 <211> 26  
 <212> DNA  
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 <220>  
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 <400> 71  
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 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Primer  
  
 <400> 72  
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 <213> Homo sapiens  
  
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 ctttagtttg cttttgcact taaaatatat ataattgact tttttggaaa aaaatctaag 120  
 attcattgct ttgttttgta aagaccaata ggttctgtat agtctttttt taaattgtgg 180  
 taaaatacac atggcattaa ttaccattt taaccattt aaagtgcaca atttgtggca 240  
 ttaagtacac tcacgttgct gtgcaaccat caccaccgtc catcttcaga acctttttat 300  
 cttcctaaac tgaaactctg tactcgtaa gcactcactt cctttttccc catccccag 360  
 ccgtagcaa ccacgactgt actttctatg aatttgacta ctctaggtac tgcattgtagg 420  
 tggaatcata cagtatttgt cttttgcttg ntttgntttg ttttttgttt tctaagacag 480  
 ggtctcactc tgcgcacctg gctggattgc agagttaagt ttatgattat gaaataaaaa 540  
 ctaaataacn attgtcctcg tttg 564  
  
 <210> 74

<211> 1161  
 <212> DNA  
 <213> Homo sapiens

<400> 74  
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 ggtttaagag gaaagctggt tcgtggggat tggatgggag gccaccagga aaccaagttc 180  
 ccgcgccagc ttcagtgtct tcctcttTcc gccgcctttg ccccgccac atcactttcg 240  
 ctccagtttt tgaaaacgct gcgaagcgga atgggtccaca ggggaaaacg gaggaggggc 300  
 caaagccagg actttgagac cggcgcgcg cgaagcccag gcagctctcc ctaaccctcc 360  
 agcactgggc aaacgctgcc cgatgacgcc cgctcgggg gccacggcat cactggggcg 420  
 actgcgagcc cggccgcgga gccgctggga cgcggcttac ctcccggctg tcgctgtgt 480  
 gtgtgtttgcc cgcgccagtc acgtccctaa tgggaccctc cgtttcggcg tctgtaaggc 540  
 gaggaggacg atgcgtcccc tccctsgcag gattgaggtt aggactaaac ggggtccgca 600  
 gcgcccggca gctcccgagc gctctcccca gccgcgcctc cctccttccc gccaccgctc 660  
 ccgcaggggc ccgcggcgct acctctcagg ctgtagcgcg cctgcatgcc gaataccgac 720  
 aggggtgccg tgcccgtgcg gtcgtccttc ctgacgcgc agcggaggat gtgttgatc 780  
 tgccccagga tttccaggtc ccagatgaag agataattct acttactgga tataggatgc 840  
 attagatctt cttaccttaa aaaaaaaaaa aaaggcagca atgatcaaaa tactaataaa 900  
 ttactcacag actcagtgt ttttttcttg gagtaaaagt ccaggatggg taatagaata 960  
 cctgctgttg gcttttgaa aaattggtac tgtatgtagc aaaataatgt gaaaccata 1020  
 tgcattgata ttcttaacaa tttgaagaaa tcgtcacagc tttcctgggt tgttgagcct 1080  
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 aaaaaaaaaa aaaaaaaaaa a 1161

<210> 75  
 <211> 123  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (1)...(123)  
 <223> Xaa = Any Amino Acid

<400> 75  
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 20 25 30  
 Val Cys Val Ala Arg Ala Ser His Val Pro Asn Gly Thr Leu Arg Phe  
 35 40 45  
 Gly Val Cys Lys Ala Arg Arg Thr Met Arg Pro Leu Pro Xaa Arg Ile  
 50 55 60  
 Glu Val Arg Thr Lys Arg Gly Pro Gln Arg Pro Ala Ala Pro Glu Arg  
 65 70 75 80  
 Ser Pro Gln Pro Arg Leu Pro Pro Ser Arg His Pro Ser Arg Arg Gly  
 85 90 95  
 Pro Arg Arg His Leu Ser Gly Cys Ser Ala Pro Ala Cys Arg Ile Pro  
 100 105 110  
 Thr Gly Cys Arg Cys Pro Cys Gly Arg Pro Ser  
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<210> 76  
 <211> 105  
 <212> PRT  
 <213> Homo sapiens

<400> 76  
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Pro Ser Leu Ala Gly Leu Arg Leu Gln Gly Val Arg Ser Ala Arg Gln  
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Leu Pro Ser Ala Leu Pro Ser Arg Ala Ser Leu Leu Pro Ala Trp Ala  
35 40 45  
Gly Arg Val Thr Ser Gln Ala Val Ala Arg Leu His Ala Glu Tyr Arg  
50 55 60  
Gln Gly Ala Gly Ala Arg Ala Val Val Leu Pro Asp Ala Ala Ala Glu  
65 70 75 80  
Asp Val Leu Asp Leu Pro Gln Asp Phe Gln Val Pro Asp Glu Glu Ile  
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100 105

<210> 77  
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<212> DNA  
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<220>  
<223> Primer

<400> 77  
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<210> 78  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 78  
ggagagctgc ctgggcttga 20

<210> 79  
<211> 23  
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<220>  
<223> Primer

<400> 79  
ttgaaaacgc tgcgaagcgg aat 23

<210> 80  
<211> 20  
<212> DNA  
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<220>  
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<400> 80  
cgctacagcc tgagaggtga 20

<210> 81  
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<212> DNA  
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 <223> Primer  
  
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 <223> Primer  
  
 <400> 83  
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 <400> 84  
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 <210> 85  
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 <212> DNA  
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 <220>  
 <223> Primer  
  
 <400> 85  
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 <210> 86  
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<400> 110  
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 <211> 289  
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 <213> Rattus

<400> 111  
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 aacttcaccg tccagaatcc tcctgaagaa ggtgctgaga gctcaaagt tatttactac 180  
 atggcagcta aagttctgca gcatctaaag ggatgttttg aaacttggtg agaatagctg 240  
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<210> 112  
 <211> 92  
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 <213> Rattus

<400> 112  
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 35 40 45  
 Glu Glu Gly Ala Glu Ser Ser Asn Val Ile Tyr Tyr Met Ala Ala Lys  
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 65 70 75 80  
 Lys Ala Leu Leu Arg Gly Val Thr Lys Lys Lys  
 85 90

<210> 113  
 <211> 1120  
 <212> DNA  
 <213> Rattus

<400> 113  
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 agcaaatgaa aatcatgatg gaaaggagag aggaggaaca cgcaaaattg atgaaagcct 180  
 tgaagaagtg caaagaagaa aagcaggagg ccagaaaact catgaacgaa gtgcaagaac 240  
 gtctggagga agaagaaaag ctatgtcagg catcttctat aggttcttgg gatggatgca 300  
 ggccatgttt ggaaagtaac tgcatacgat tttatacagc ttgccaacct ggttggtcct 360  
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 gtgaagatgt aaaggatccc cctgccatag aacagctgac taaggaagat ttacaagtgg 480  
 tacacataga gaacctgttt agccagctgg ccgtggatgc aaaatctctc ttcaacatga 540  
 gctttttacat ttttaagcag atgcagcaag aatttgatca ggcttttcaa ttatacttca 600  
 tgtccgatgt ggacttaatg gagccatacc cccagctttt atctaaagag ataatcaaaa 660  
 aagaagaact tgggcaaagg tggggcattc ccaatgtctt ccagctgttt cataatttca 720

gtctctctgt	ttatgggaga	gtccaacaaa	taataatgaa	gacactcaat	gcaattgaag	780
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agcaaaatgg	agaaatgtgt	gaggaatttg	tcaagaattt	atctggatgt	ttaaaatttc	900
gtaaaagatg	ccaaaaatgt	cacaattacc	tatctgaaga	atgccctgat	gtacctgaac	960
ttcacataga	attccttgag	gccctgaaat	tagtcaatgt	atccaatcag	caatatgatc	1020
agattgtcca	gatgaccocag	tatcatttgg	aagataccat	atacctgatg	gagaaaaatgc	1080
aagagcagtt	tggatgggtg	tctcaactgg	caagccataa			1120

<210> 114  
 <211> 397  
 <212> PRT  
 <213> Rattus

<400> 114

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			20					25					30		
Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg
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	50					55					60				
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Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val
145					150					155					160
His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu
			165						170					175	
Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp
		180						185					190		
Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro
	195						200					205			
Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly
	210					215					220				
Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser
225					230					235					240
Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn
			245					250						255	
Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly
		260						265					270		
Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu
		275					280					285			
Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln
	290					295					300				
Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu
305					310					315					320
His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln
			325						330					335	
Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr
		340						345					350		
Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln
	355					360					365				
Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys
	370					375					380				

Ala Val Pro Lys Ile His Gly Gly Asp Ser Ser Lys Gln  
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<210> 115  
 <211> 341  
 <212> DNA  
 <213> Rattus

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 gcctctccta cctctggaag actcttttagg ttccatccg tagcatctgt ctctttccaa 180  
 gtaggtgcac tgtcacaata tttcaacct aacagatata cagaaatcac aaagagtggg 240  
 ggctgcatgg tccagtgttc caccgatatt gcagctctcc ccagagaaat tgccactaac 300  
 ttctgaaagg accttcactt tttacgatgt gcctcgtgcc g 341

<210> 116  
 <211> 341  
 <212> DNA  
 <213> Rattus

<400> 116  
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 gggagagctg caatatcggt ggaacactgg accatgcagc caccactctt tgtgatttct 120  
 gtgtatctgt tatggttgaa atattgtgac agtgcaccta cttggaagga gacagatgct 180  
 acggatggaa acctaaagag tcttcagag gtaggagagg cagatgtaga gggagaggtc 240  
 aagaaggctt tgattggcat taagcaaag aaaatcatga tggaaaggag agaggaggaa 300  
 caccgaaaat tgatgaaagc cttgaaaaaa aaaaaaaaaa a 341

<210> 117  
 <211> 112  
 <212> PRT  
 <213> Rattus

<400> 117  
 Arg His Glu Ala His Arg Lys Lys Arg Ser Phe Gln Lys Leu Val Ala  
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 20 25 30  
 Pro Pro Leu Phe Val Ile Ser Val Tyr Leu Leu Trp Leu Lys Tyr Cys  
 35 40 45  
 Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly Asn Leu  
 50 55 60  
 Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu Val Lys  
 65 70 75 80  
 Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Arg  
 85 90 95  
 Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Lys Lys Lys  
 100 105 110

<210> 118  
 <211> 56  
 <212> PRT  
 <213> Rattus

<400> 118  
 Thr Asp Ala Thr Asp Gly Asn Leu Lys Ser Leu Pro Glu Val Gly Glu  
 1 5 10 15  
 Ala Asp Val Glu Gly Glu Val Lys Lys Ala Leu Ile Gly Ile Lys Gln  
 20 25 30  
 Met Lys Ile Met Met Glu Arg Arg Glu Glu Glu His Ala Lys Leu Met  
 35 40 45

Lys Ala Leu Lys Lys Lys Lys Lys  
50 55

<210> 119  
<211> 1545  
<212> DNA  
<213> Rattus

<400> 119  
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gtgtatctgt tatggtgaaa tattgtgaca gtgcacctac ttggaaggag acagatgcta 180  
cggatggaaa cctaaagagt cttccagagg taggagagggc agatgtagag ggagaggtca 240  
agaaggcttt gattggcatt aagcaaataa aaatcatgat ggaaaggaga gaggaggaaac 300  
acgcaaaatt gatgaaagcc ttgaagaagt gcaaagaaga aaagcaggag gccagaaac 360  
tcatgaacga agtgcaagaa cgtctggagg aagaagaaaa gctatgtcag gcatcttcta 420  
taggttcttg ggatggatgc aggccatgtt tggaaagtaa ctgcatacga tttatacacg 480  
cttgccaacc tggttggtcc tctgtgaaaa gcatgatgaa gcaatttctc aagaagatat 540  
accgatttct gtcttccag agtgaagatg taaaggatcc ccctgccata gaacagctga 600  
ctaaggaaga tttacaagtg gtacacatag agaacctgtt tagccagctg gccgtggatg 660  
caaaatctct cttcaacatg agcttttaca tttttaagca gatgcagcaa gaatttgatc 720  
aggcttttca attatacttc atgtccgatg tggacttaac ggagccatac cccccagctt 780  
tatctaaaga gataatcaaa aaagaagaac ttggggcaag gtggggcatt cccaatgtct 840  
tccagctgtt tcataatttc agtctctctg tttatgggag agtccaacaa ataataatga 900  
agacactcaa tgcaattgaa gattcatggg aaccacacaa agagttagac cagagaggta 960  
tgacttcaga gatgttacct gagcaaaatg gagaaatgtg tgaggaattt gtcaagaatt 1020  
tatctggatg tttaaaattt cgtaaaagat gccaaaaatg tcacaattac ctatctgaag 1080  
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tatacctgat ggagaaaatg caagagcagt ttggatgggt gtctcaactg gcaagccata 1260  
accagtgac tgaggacatc ttttaattcaa caaaggcagt tccaaagatt catggaggag 1320  
attcttccaa gcaggatgaa attatggtag actcaagcag cattctgcct tcctctaact 1380  
tcaccgtcca gaatcctcct gaagaagggtg ctgagagctc aaatgttatt tactacatgg 1440  
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ggaaagcttt gttgagaggg taggtaacat aaaaaaaaaa aaaaa 1545

<210> 120  
<211> 512  
<212> PRT  
<213> Rattus

<400> 120  
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20 25 30  
Ala Thr Thr Leu Cys Asp Phe Cys Val Ser Val Met Val Lys Tyr Cys  
35 40 45  
Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly Asn Leu  
50 55 60  
Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu Val Lys  
65 70 75 80  
Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Arg  
85 90 95  
Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Cys Lys Glu  
100 105 110  
Glu Lys Gln Glu Ala Gln Lys Leu Met Asn Glu Val Gln Glu Arg Leu  
115 120 125  
Glu Glu Glu Glu Lys Leu Cys Gln Ala Ser Ser Ile Gly Ser Trp Asp  
130 135 140  
Gly Cys Arg Pro Cys Leu Glu Ser Asn Cys Ile Arg Phe Tyr Thr Ala  
145 150 155 160

Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	Phe	Leu	
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Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	Lys	Asp	
			180					185					190			
Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val	His	
		195					200					205				
Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu	Phe	
	210					215					220					
Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln	
225					230					235					240	
Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro	Tyr	
			245						250					255		
Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly	Gln	
		260						265					270			
Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser	Leu	
		275					280					285				
Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn	Ala	
	290					295					300					
Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly	Met	
305					310					315					320	
Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu	Phe	
				325					330						335	
Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln	Lys	
			340					345					350			
Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu	His	
		355					360					365				
Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln	Gln	
	370					375					380					
Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr	Ile	
385					390					395					400	
Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln	Leu	
			405						410					415		
Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys	Ala	
			420					425					430			
Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu	Ile	Met	
		435					440					445				
Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val	Gln	Asn	
	450					455					460					
Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr	Met	Ala	
465					470					475					480	
Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp	Glu	Leu	
				485					490					495		
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			500					505					510			

<210> 121  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<400> 121  
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 cagatgaccc ggaagcactt ggaggacacc gcctatctgg tggagaagat gagagggcaa 120  
 tttggctggg tgtctgaact ggcaaaccag gccccagaaa cagagatcat cttaattca 180  
 atacaggtaa gaagatctaa tgcatcctat atccagtaag t 221

<210> 122  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

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<400> 122
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ggcaatttgg ctgggtgtct gaactggcaa accaggcccc agaaacagag atcatcttta      180
attcaataca ggtagtcca aggattcatg aaggaaatat ttccaaacaa gatgaaacaa      240
tgatgacaga cttaaagcatt ctgccttcct ctaatttcac actcaagatc cctcttgaag      300
aaagtgtga gagttctaac ttcatgggt acgtagtggc aaaagctcta cagcatttta      360
aggaacattt taaaacctgg taagcagagt gcctggttag gaatgccttg ttgacaggaa      420
tagttaattc tcaaaagggg aaaacaaaac ttgtttcaaa atacctggaa aacatgttta      480
acctcattaa taaagacatg aaaacaaaac agatggcatt ttct                                524

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<210> 123
<211> 568
<212> DNA
<213> Homo sapiens

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<400> 123
gaattagacg aggcgatcag gttgggtcaat gtatccaatc agcagtatgg ccagattctc      60
cagatgaccc ggaagcactt ggaggacacc gcctatctgg tggagaagat gagagggcaa      120
tttggttggg tgtctgaact ggcaaaccag gcccagaaa cagagatcat ctttaattca      180
atacaggtag ttccaaggat tcatgaagga aatatttcca aacaagatga aacaatgatg      240
acagacttaa gcattctgcc ttctctaat ttcacactca agatccctct tgaagaaagt      300
gctgagagtt ctaacttcat tggctacgta gtggcaaaag ctctacagca ttttaaggaa      360
cattttaaaa cctgaaaaag atcctgaggg tcagtgtcca aggtccaatg aactactcag      420
gtcggaggtg gtagagcagc atgtggagcc agttctctct ccgactccat catcacactg      480
cacggcttcc tgtaagata tttgtcaaa aaatgcgaga tataaaaatc tgggtaagaa      540
gatctaattg atcctatatc cagtaagt                                568

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```

<210> 124
<211> 1141
<212> DNA
<213> H. sapiens

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<220>
<221> misc feature
<222> (789)...(798)
<223> additional sequence present in full genomic sequence

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<400> 124
cctgaaagcc tggcgccaat gaccgcgag acattttttg cctgggggtgc tcctgtcgga      60
aaggaaagag gaaaggacga ctaagaactt atactcgaac tcccgaattt ctcttttcaa      120
ggtttaagag gaaagctggt tcgtggggat tggatgggag gccaccagga aaccaagttc      180
ccgcgccagc ttcagtgtct tcctcttycc gccgcctttg ccccgccac atcactttcg      240
ctccagtttt tgaaaacgct gcgaagcgga atggtccaca ggggaaaacg gaggaggggc      300
caaagccagg actttgagac cggcgcgcgg tcaagccag gcagctctcc ctaaccctcc      360
agcactgggc aaacgctgcc cgatgacgcc cgctcgggg gccacggcat cactggggcg      420
actgcgagcc cggcgcgga gccgctggga cgcggcttac ctcccggtg tcgctgctgt      480
gtgtgttgcc cgcgccagtc acgtccctaa tgggaccctc cgtttcggcg tctgtaaggc      540
gaggaggacg atgcgtcccc tccctsgcag gattgaggtt aggactaaac ggggtccgca      600
gcgcccggca gctcccgagc gctctcccca gccgcgcctc cctccttccc gccaccgctc      660
ccgcaggggc ccgcggcgct acctctcagg ctgtagcgcg cctgcatgcc gaataccgac      720
agggtgccgg tgcccgtgcg gtcgtccttc ctgacgcgcg agcggaggat gtgttgatc      780
tgccccaggt actttcagga ttccaggctc ccagatgaag agataattct acttactgga      840
tataggatgc attagatctt cttaccttaa aaaaaaaaaa aaaggcagca atgatcaaaa      900
tactaataaa ttactcacag actcagtgtt tttttcttg gagtaaaagt ccaggatggg      960
taatagaata cctgctgttg gcttttgga aaattggtac tgtatgtagc aaaataatgt      1020
gaaaccata tgcattgata ttcttaacaa tttgaagaaa tcgtcacagc tttcctgggt      1080
tgttgagcct ctaaaatggt ctttctctct gatgtgataa taaagtgttt attttgaact      1140
c                                                                1141

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<210> 125
<211> 27

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<212> PRT  
 <213> Homo sapiens

<400> 125  
 Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys Leu  
 1 5 10 15  
 Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
 20 25

<210> 126  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<400> 126  
 Gly Glu Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys  
 1 5 10 15  
 Cys Gln Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro  
 20 25

<210> 127  
 <211> 27  
 <212> PRT  
 <213> Cavia sp.

<400> 127  
 Cys Gln Val Ser Leu Ala Asp Ser Trp Asp Glu Cys Arg Ala Cys Leu  
 1 5 10 15  
 Glu Ser Asn Cys Met Arg Phe Asp Thr Thr Cys  
 20 25

<210> 128  
 <211> 30  
 <212> PRT  
 <213> Cavia sp.

<400> 128  
 Asp Gly Lys Leu Gly Gln Asn Leu Ser Asp Cys Val Asn Phe Arg Lys  
 1 5 10 15  
 Arg Cys Gln Lys Cys Gln Asp Tyr Leu Ser Asp Asp Cys Pro  
 20 25 30

<210> 129  
 <211> 27  
 <212> PRT  
 <213> Bos sp.

<400> 129  
 Cys Gln Val Ser Leu Met Gly Ser Trp Asp Glu Cys Lys Ser Cys Leu  
 1 5 10 15  
 Glu Ser Asp Cys Met Arg Phe Tyr Thr Thr Cys  
 20 25

<210> 130  
 <211> 29  
 <212> PRT  
 <213> Bos sp.

<400> 130  
 Leu Cys Gly Glu Pro Gly Gln Asn Ser Ser Glu Cys Leu Gln Phe His  
 1 5 10 15  
 Ala Arg Cys Gln Lys Cys Gln Asp Tyr Leu Trp Ala Asp

<210> 131  
 <211> 30  
 <212> PRT  
 <213> Homo sapiens

<400> 131  
 Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg Ser Cys Leu  
 1 5 10 15  
 Glu Asn Asn Cys Met Arg Ile Tyr Thr Cys Cys Gly Glu  
 20 25 30

<210> 132  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Arg Arg Ser Asn Ala Ser Tyr Ile Gln  
 1 5

<210> 133  
 <211> 494  
 <212> PRT  
 <213> Homo sapiens

<400> 133  
 Met Lys Ile Lys Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp  
 1 5 10 15  
 Gln Leu His Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro  
 20 25 30  
 Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His  
 35 40 45  
 Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys  
 50 55 60  
 Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys  
 65 70 75 80  
 Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu  
 85 90 95  
 Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu  
 100 105 110  
 Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu  
 115 120 125  
 Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu  
 130 135 140  
 Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
 145 150 155 160  
 Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg  
 165 170 175  
 Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp  
 180 185 190  
 Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln  
 195 200 205  
 Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe  
 210 215 220  
 Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln  
 225 230 235 240  
 Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr  
 245 250 255  
 Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu  
 260 265 270

Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser  
 275 280 285  
 Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys  
 290 295 300  
 Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly  
 305 310 315 320  
 Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu  
 325 330 335  
 Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln  
 340 345 350  
 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
 355 360 365  
 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln  
 370 375 380  
 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr  
 385 390 395 400  
 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
 405 410 415  
 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln  
 420 425 430  
 Val Val Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr  
 435 440 445  
 Met Met Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys  
 450 455 460  
 Ile Pro Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val  
 465 470 475 480  
 Val Ala Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr  
 485 490

<210> 134  
 <211> 1541  
 <212> DNA  
 <213> Rattus

<400> 134  
 aaaacgacgg ccagtgcggc acgaggcaca tcgtaaaaag tgaaggtcct ttcagaagtt 60  
 agtggcaatt tctctgggga gagctgcaat atcgggtggaa cactggacca tgcagccacc 120  
 actctttgtg atttctgtgt atctgttatg gttgaaatat tgtgacagtg cacctacttg 180  
 gaaggagaca gatgctacgg atggaaacct aaagagtctt ccagaggtag gagaggcaga 240  
 tgtagaggga gaggtcaaga aggctttgat tggcattaag caaatgaaaa tcatgatgga 300  
 aaggagagag gaggaacacg caaaattgat gaaagccttg aagaagtgca aagaagaaaa 360  
 gcaggaggcc cagaaactca tgaacgaagt gcaagaacgt ctggaggaag aagaaaagct 420  
 atgtcaggca tcttctatag gttcttgga tggatgcagg ccatgtttgg aaagtaactg 480  
 catacgattt tatacagctt gccaacctgg ttggtcctct gtgaaaagca tgatgaagca 540  
 atttctcaag aagatatacc gatttctgtc ttcccagagt gaagatgtaa aggatcccc 600  
 tgccatagaa cagctgacta aggaagattt acaagtggta cacatagaga acctgtttag 660  
 ccagctggcc gtggatgcaa aatctctctt caacatgagc ttttacattt ttaagcagat 720  
 gcagcaagaa tttgatcagg cttttcaatt atacttcag tccgatgtgg acttaatgga 780  
 gccatacccc ccagctttat cttaaagagat aatcaaaaaa gaagaacttg ggcaaagggtg 840  
 gggcattccc aatgtcttcc agctgtttca taatttcagt ctctctgttt atgggagagt 900  
 ccaacaaata ataatgaaga cactcaatgc aattgaagat tcatgggaac cacacaaaga 960  
 gttagaccag agaggatga cttcagagat gttacctgag caaaatggag aaatgtgtga 1020  
 ggaatttgtc aagaatttat ctggatgttt aaaatttcgt aaaagatgcc aaaaatgtca 1080  
 caattaccta tctgaagaat gccctgatgt acctgaactt cacatagaat tccttgaggc 1140  
 cctgaaatta gtcaatgtat ccaatcagca atatgatcag attgtccaga tgaccagta 1200  
 tcatttgga gataccatat acctgatgga gaaaatgcaa gagcagtttg gatgggtgtc 1260  
 tcaactggca agccataacc cagtactga ggacatcttt aattcaacaa aggcagttcc 1320  
 aaagattcat ggaggagatt cttccaagca ggatgaaatt atggtagact caagcagcat 1380  
 tctgccttcc tctaacttca ccgtccagaa tcctcctgaa gaaggtgctg agagctcaaa 1440  
 tgttatttac tacatggcag cttaaagttct gcagcatcta aagggtgtt ttgaaacttg 1500  
 gtaagaatag ctgattagga aagctttgtt gagagggtag g 1541

<210> 135  
 <211> 464  
 <212> PRT  
 <213> Rattus

<400> 135

Met	Gln	Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys
1				5					10					15	
Tyr	Cys	Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly
			20					25					30		
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu
		35					40					45			
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
	50					55					60				
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys
65					70					75					80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu
				85				90						95	
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser
				100				105					110		
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr
	115						120					125			
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln
	130					135					140				
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val
145					150					155					160
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val
				165				170						175	
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser
			180					185					190		
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe
	195						200					205			
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu
	210					215				220					
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu
225					230					235					240
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe
				245				250						255	
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu
			260					265					270		
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg
	275						280					285			
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu
	290					295					300				
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys
305					310					315					320
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu
				325				330						335	
Leu	His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn
			340					345					350		
Gln	Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp
		355					360					365			
Thr	Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser
	370					375					380				
Gln	Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr
385					390					395					400
Lys	Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu
				405				410						415	
Ile	Met	Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val
			420					425					430		
Gln	Asn	Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr

435 440 445  
Met Ala Ala Lys Val Leu Gln His Leu Lys Gly Cys Phe Glu Thr Trp  
450 455 460

<210> 136  
<211> 1541  
<212> DNA  
<213> Rattus

<400> 136  
aaaacgacgg ccagtgcggc acgaggcaca tcgtaaaaag tgaaggctct ttcagaagtt 60  
agtggcaatt tctctgggga gagctgcaat atcggtggaa cactggacca tgcagccacc 120  
actctttgtg atttctgtgt atctgttatg gttgaaatat tgtgacagtg cacctacttg 180  
gaaggagaca gatgctacgg atggaaacct aaagagtctt ccagaggtag gagaggcaga 240  
tgtagaggga gaggtcaaga aggctttgat tggcattaag caaatgaaaa tcatgatgga 300  
aaggagagag gaggaacacg caaaattgat gaaagccttg aagaagtgca aagaagaaaa 360  
gcaggaggcc cagaaactca tgaacgaagt gcaagaacgt ctggagggaag aagaaaagct 420  
atgtcaggca tcttctatag gttcttggga tggatgcagg ccatgttttg aaagtaactg 480  
catacgattt tatacagctt gccaacctgg ttggtcctct gtgaaaagca tgatgaagca 540  
atttctcaag aagatatacc gatttctgtc ttcccagagt gaagatgtaa aggatcccc 600  
tgccatagaa cagctgacta aggaagattt acaagtggta cacatagaga acctgttttag 660  
ccagctggcc gtggatgcaa aatctctctt caacatgagc ttttacattt ttaagcagat 720  
gcagcaagaa tttgatcagg cttttcaatt atacttcatg tccgatgtgg acttaatgga 780  
gccatacccc ccagctttat cttaaagagat aatcaaaaaa gaagaacttg ggcaaagggtg 840  
gggcattccc aatgtcttcc agctgtttca taatttcagt ctctctgttt atgggagagt 900  
ccaacaaata ataatgaaga cactcaatgc aattgaagat tcatgggaac cacacaaaga 960  
gtagaccag agaggtatga cttcagagat gttacctgag caaatggag aaatgtgtga 1020  
ggaatttgtc aagaatttat ctggatgttt aaaatttcgt aaaagatgcc aaaaatgtca 1080  
caattaccta tctgaagaat gccctgatgt acctgaactt cacatagaat tccttgaggc 1140  
cctgaaatta gtcaatgtat ccaatcagca atatgatcag attgtccaga tgaccagta 1200  
tcatttgga gataccatat acctgatgga gaaaatgcaa gaggcagttt gatgggtgtc 1260  
tcaactggca agccataacc cagtgactga ggacatcttt aattcaacaa aggcagttcc 1320  
aaagattcat ggaggagatt cttccaagca ggatgaaatt atggtagact caagcagcat 1380  
tctgccttcc tctaacttca ccgtccagaa tcctcctgaa gaagggtgtg agagctcaaa 1440  
tgttatttac tacatggcag ctaaagttct gcagcatcta aagggatgtt ttgaaacttg 1500  
gtaagaatag ctgattagga aagctttgtt gagagggtag g 1541

<210> 137  
<211> 464  
<212> PRT  
<213> Rattus

<400> 137  
Met Gln Pro Pro Leu Phe Val Ile Ser Val Tyr Leu Leu Trp Leu Lys  
1 5 10 15  
Tyr Cys Asp Ser Ala Pro Thr Trp Lys Glu Thr Asp Ala Thr Asp Gly  
20 25 30  
Asn Leu Lys Ser Leu Pro Glu Val Gly Glu Ala Asp Val Glu Gly Glu  
35 40 45  
Val Lys Lys Ala Leu Ile Gly Ile Lys Gln Met Lys Ile Met Met Glu  
50 55 60  
Arg Arg Glu Glu Glu His Ala Lys Leu Met Lys Ala Leu Lys Lys Cys  
65 70 75 80  
Lys Glu Glu Lys Gln Glu Ala Gln Lys Leu Met Asn Glu Val Gln Glu  
85 90 95  
Arg Leu Glu Glu Glu Glu Lys Leu Cys Gln Ala Ser Ser Ile Gly Ser  
100 105 110  
Trp Asp Gly Cys Arg Pro Cys Leu Glu Ser Asn Cys Ile Arg Phe Tyr  
115 120 125  
Thr Ala Cys Gln Pro Gly Trp Ser Ser Val Lys Ser Met Met Lys Gln  
130 135 140  
Phe Leu Lys Lys Ile Tyr Arg Phe Leu Ser Ser Gln Ser Glu Asp Val

145		150		155		160
Lys Asp Pro Pro Ala	Ile Glu Gln Leu Thr	Lys Glu Asp Leu Gln Val				
	165	170		175		
Val His Ile Glu Asn	Leu Phe Ser Gln Leu Ala	Val Asp Ala Lys Ser				
	180	185		190		
Leu Phe Asn Met Ser	Phe Tyr Ile Phe Lys Gln Met	Gln Gln Glu Phe				
	195	200		205		
Asp Gln Ala Phe Gln	Leu Tyr Phe Met Ser Asp	Val Asp Leu Met Glu				
	210	215		220		
Pro Tyr Pro Pro Ala	Leu Ser Lys Glu Ile Thr	Lys Lys Glu Glu Leu				
	225	230		235		240
Gly Gln Arg Trp Gly	Ile Pro Asn Val Phe Gln	Leu Phe His Asn Phe				
	245	250		255		
Ser Leu Ser Val Tyr	Gly Arg Val Gln Gln Ile	Ile Met Lys Thr Leu				
	260	265		270		
Asn Ala Ile Glu Asp	Ser Trp Glu Pro His Lys	Glu Leu Asp Gln Arg				
	275	280		285		
Gly Met Thr Ser Glu	Met Leu Pro Glu Gln Asn	Gly Glu Met Cys Glu				
	290	295		300		
Glu Phe Val Lys Asn	Leu Ser Gly Cys Leu Lys	Phe Arg Lys Arg Cys				
	305	310		315		320
Gln Lys Cys His Asn	Tyr Leu Ser Glu Glu Cys	Pro Asp Val Pro Glu				
	325	330		335		
Leu His Ile Glu Phe	Leu Glu Ala Leu Lys	Leu Val Asn Val Ser Asn				
	340	345		350		
Gln Gln Tyr Asp Gln	Ile Val Gln Met Thr	Gln Tyr His Leu Glu Asp				
	355	360		365		
Thr Ile Tyr Leu Met	Glu Lys Met Gln Glu Gln	Phe Gly Trp Val Ser				
	370	375		380		
Gln Leu Ala Ser His	Asn Pro Val Thr Glu Asp	Ile Phe Asn Ser Thr				
	385	390		395		400
Lys Ala Val Pro Lys	Ile His Gly Gly Asp Ser	Ser Lys Gln Asp Glu				
	405	410		415		
Ile Met Val Asp Ser	Ser Ser Ile Leu Pro Ser	Ser Asn Phe Thr Val				
	420	425		430		
Gln Asn Pro Pro Glu	Glu Gly Ala Glu Ser Ser	Asn Val Ile Tyr Tyr				
	435	440		445		
Met Ala Ala Lys Val	Leu Gln His Leu Lys Gly	Cys Phe Glu Thr Trp				
	450	455		460		

<210> 138  
 <211> 1326  
 <212> DNA  
 <213> Rattus

<400> 138	
aaaacgacgg ccagtgcggc acgaggcaca tcgtaaaaag tgaaggctct ttcagaagtt	60
agtggcaatt tctctgggga gagctgcaat atcggtggaa cactggacca tgcagccacc	120
actctttgtg atttctgtgt atctgttatg gttgaaatat tgtgacagtg cacctacttg	180
gaaggagaca gatgctacgg atggaaacct aaagagtctt ccagaggtag gagaggcaga	240
tgtagaggga gaggtcaaga aggcctttgat tggcattaag caaatgaaaa tcatgatgga	300
aaggagagag gaggaacacg caaaattgat gaaagccttg aagaagtgca aagaagaaaa	360
gcaggaggcc cagaaactca tgaacgaagt gcaagaacgt ctggagggaag aagaaaagct	420
atgtcaggca tcttctatat gttcttgagg tggatgcagg ccatgttttg aaagtaactg	480
catacgattt tatacagctt gccaacctgg ttggtcctct gtgaaaagca tgatgaagca	540
atttctcaag aagatatacc gatttctgtc ttcccagagt gaagatgtaa aggatcccc	600
tgccatagaa cagctgacta aggaagattt acaagtggta cacatagaga acctgtttag	660
ccagctggcc gtggatgcaa aatctctctt caacatgagc ttttacattt ttaagcagat	720
gcagcaagaa tttgatcagg cttttcaatt atacttcatg tccgatgtgg acttaatgga	780
gccatacccc ccagctttat cttaaagagat aacaaaaaaa gaagaacttg ggcaaagggtg	840
gggcattccc aatgtcttcc agctgtttca taatttcagt ctctctgttt atgggagagt	900
ccaacaaata ataatgaaga cactcaatgc aattgaagat tcatgggaac cacacaaaga	960

gtagaccag	agaggtatga	cttcagagat	gttacctgag	caaaatggag	aaatgtgtga	1020
ggaatttgtc	aagaatttat	ctggatgttt	aaaatttcgt	aaaagatgcc	aaaaatgtca	1080
caattaccta	tctgaaggca	gttccaaaga	ttcatggagg	agattcttcc	aagcaggatg	1140
aaattatggt	agactcaagc	agcattctgc	cttcctctaa	cttcaccgtc	cagaatcctc	1200
ctgaagaagg	tgctgagagc	tcaaagtgtta	tttactacat	ggcagctaaa	gttctgcagc	1260
atctaaaggg	atgttttgaa	acttggttaag	aatagctgat	taggaaagct	ttgttgagag	1320
ggtagg						1326

<210> 139

<211> 344

<212> PRT

<213> Rattus

<400> 139

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<210> 140

<211> 18596

<212> DNA  
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<400> 140

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 ctccgtgtgc ctttcaacat cgccagctac gccctgtcga cgtacatgat tgcgcacatc 720  
 acgggcctga agccagggtga ctttatacac actttgggag atgcacatat ttacctgaat 780  
 cacatcgagc cactgaaaat tcagcttcag cgagaaccca gacctttccc aaagctcagg 840  
 attcttcgaa aagttgagaa aattgatgac ttcaaagctg aagactttca gattgaaggg 900  
 tacaatccgc atccaactat taaaatggaa atggctgttt ag 942

<210> 144  
 <211> 186  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Pro Val Ala Gly Ser Glu Leu Pro Arg Arg Pro Leu Pro Pro Ala  
 1 5 10 15  
 Ala Gln Glu Arg Asp Ala Glu Pro Arg Pro Pro His Gly Glu Leu Gln  
 20 25 30  
 Tyr Leu Gly Gln Ile Gln His Ile Leu Arg Cys Gly Val Arg Lys Asp  
 35 40 45

Asp	Arg	Thr	Gly	Thr	Gly	Thr	Leu	Ser	Val	Phe	Gly	Met	Gln	Ala	Arg	
50						55					60					
Tyr	Ser	Leu	Arg	Asp	Glu	Phe	Pro	Leu	Leu	Thr	Thr	Lys	Arg	Val	Phe	
65					70					75					80	
Trp	Lys	Gly	Val	Leu	Glu	Glu	Leu	Leu	Trp	Phe	Ile	Lys	Gly	Ser	Thr	
				85					90					95		
Asn	Ala	Lys	Glu	Leu	Ser	Ser	Lys	Gly	Val	Lys	Ile	Trp	Asp	Ala	Asn	
			100					105					110			
Gly	Ser	Arg	Asp	Phe	Leu	Asp	Ser	Leu	Gly	Phe	Ser	Thr	Arg	Glu	Glu	
		115					120					125				
Gly	Asp	Leu	Gly	Pro	Val	Tyr	Gly	Phe	Gln	Trp	Arg	His	Phe	Gly	Ala	
130						135				140						
Glu	Tyr	Arg	Asp	Met	Glu	Ser	Asp	Tyr	Ser	Gly	Gln	Gly	Val	Asp	Gln	
145					150					155					160	
Leu	Gln	Arg	Val	Ile	Asp	Thr	Ile	Lys	Thr	Asn	Pro	Asp	Asp	Arg	Arg	
				165					170						175	
Ile	Ile	Met	Cys	Ala	Trp	Asn	Pro	Arg	Asp							
			180					185								

<210> 145  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

Lys	Pro	Gly	Asp	Phe	Ile	His	Thr	Leu	Gly	Asp	Ala	His	Ile	Tyr	Leu	
1				5					10					15		
Asn	His	Ile	Glu	Pro	Leu	Lys	Ile	Gln	Leu	Gln	Arg	Glu	Pro	Arg	Pro	
			20					25					30			
Phe	Pro	Lys	Leu	Arg	Ile	Leu	Arg	Lys	Val	Glu	Lys	Ile	Asp	Asp	Phe	
		35					40					45				
Lys	Ala	Glu	Asp	Phe	Gln	Ile	Glu	Gly	Tyr	Asn	Pro	His	Pro	Thr	Ile	
50						55					60					
Lys	Met	Glu	Met	Ala	Val											
65					70											

<210> 146  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

Leu	Pro	Leu	Met	Ala	Leu	Pro	Pro	Cys	His	Ala	Leu	Cys	Gln	Phe	Tyr	
1				5					10					15		
Val	Val															

<210> 147  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

Met	Gly	Leu	Gly	Val	Pro	Phe	Asn	Ile	Ala	Ser	Tyr	Ala	Leu	Leu	Thr	
1				5					10					15		
Tyr	Met	Ile	Ala	His	Ile	Thr	Gly	Leu								
			20					25								

<210> 148  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 148

Asn Ser Glu Leu Ser Cys Gln Leu Tyr Gln Arg Ser Gly Asp  
1 5 10

<210> 149

<211> 14

<212> PRT

<213> Homo sapiens

<400> 149

Asn Ser Glu Leu Ser Cys Gln Leu Tyr Gln Arg Ser Gly Asp  
1 5 10

<210> 150

<211> 18

<212> PRT

<213> Homo sapiens

<400> 150

Leu Pro Leu Met Ala Leu Pro Pro Cys His Ala Leu Cys Gln Phe Tyr  
1 5 10 15  
Val Val

<210> 151

<211> 25

<212> PRT

<213> Homo sapiens

<400> 151

Met Gly Leu Gly Val Pro Phe Asn Ile Ala Ser Tyr Ala Leu Leu Thr  
1 5 10 15  
Tyr Met Ile Ala His Ile Thr Gly Leu  
20 25

<210> 152

<211> 186

<212> PRT

<213> Homo sapiens

<400> 152

Met Pro Val Ala Gly Ser Glu Leu Pro Arg Arg Pro Leu Pro Pro Ala  
1 5 10 15  
Ala Gln Glu Arg Asp Ala Glu Pro Arg Pro Pro His Gly Glu Leu Gln  
20 25 30  
Tyr Leu Gly Gln Ile Gln His Ile Leu Arg Cys Gly Val Arg Lys Asp  
35 40 45  
Asp Arg Thr Gly Thr Gly Thr Leu Ser Val Phe Gly Met Gln Ala Arg  
50 55 60  
Tyr Ser Leu Arg Asp Glu Phe Pro Leu Leu Thr Thr Lys Arg Val Phe  
65 70 75 80  
Trp Lys Gly Val Leu Glu Glu Leu Leu Trp Phe Ile Lys Gly Ser Thr  
85 90 95  
Asn Ala Lys Glu Leu Ser Ser Lys Gly Val Lys Ile Trp Asp Ala Asn  
100 105 110  
Gly Ser Arg Asp Phe Leu Asp Ser Leu Gly Phe Ser Thr Arg Glu Glu  
115 120 125  
Gly Asp Leu Gly Pro Val Tyr Gly Phe Gln Trp Arg His Phe Gly Ala  
130 135 140



Glu Tyr Arg Asp Met Glu Ser Asp Tyr Ser Gly Gln Gly Val Asp Gln  
 145 150 155 160  
 Leu Gln Arg Val Ile Asp Thr Ile Lys Thr Asn Pro Asp Asp Arg Arg  
 165 170 175  
 Ile Ile Met Cys Ala Trp Asn Pro Arg Asp  
 180 185

<210> 153  
 <211> 70  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Lys Pro Gly Asp Phe Ile His Thr Leu Gly Asp Ala His Ile Tyr Leu  
 1 5 10 15  
 Asn His Ile Glu Pro Leu Lys Ile Gln Leu Gln Arg Glu Pro Arg Pro  
 20 25 30  
 Phe Pro Lys Leu Arg Ile Leu Arg Lys Val Glu Lys Ile Asp Asp Phe  
 35 40 45  
 Lys Ala Glu Asp Phe Gln Ile Glu Gly Tyr Asn Pro His Pro Thr Ile  
 50 55 60  
 Lys Met Glu Met Ala Val  
 65 70

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<400> 154  
 gtcattgcttt tatacattct ggc 23

<210> 155  
 <211> 25  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
 ttattctgttt agatcagcac tacac 25

<210> 156  
 <211> 28  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 gtacttgata tttatataca tcctaatac 28

<210> 157  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 gtaatccaac actttgggag g 21

<210> 158  
 <211> 70  
 <212> PRT

<213> Homo sapiens

<400> 158

Lys Pro Gly Asp Phe Ile His Thr Leu Gly Asp Ala His Ile Tyr Leu  
1 5 10 15  
Asn His Ile Glu Pro Leu Lys Ile Gln Leu Gln Arg Glu Pro Arg Pro  
20 25 30  
Phe Pro Lys Leu Arg Ile Leu Arg Lys Val Glu Lys Ile Asp Asp Phe  
35 40 45  
Lys Ala Glu Asp Phe Gln Ile Glu Gly Tyr Asn Pro His Pro Thr Ile  
50 55 60  
Lys Met Glu Met Ala Val  
65 70

<210> 159

<211> 437

<212> PRT

<213> H. sapiens

<400> 159

Met Lys Ile Lys Ala Glu Lys Asn Glu Gly Pro Ser Arg Ser Trp Trp  
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Gln Leu His Trp Gly Asp Ile Ala Asn Asn Ser Gly Asn Met Lys Pro  
20 25 30  
Pro Leu Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His  
35 40 45  
Cys Ala Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys  
50 55 60  
Ser Phe Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys  
65 70 75 80  
Ala Leu Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu  
85 90 95  
Lys Glu His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu  
100 105 110  
Lys Gln Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu  
115 120 125  
Glu Glu Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu  
130 135 140  
Cys Arg Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys  
145 150 155 160  
Gln Pro Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg  
165 170 175  
Lys Ile Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp  
180 185 190  
Leu Pro Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln  
195 200 205  
Met Glu Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe  
210 215 220  
Asn Arg Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln  
225 230 235 240  
Thr Phe Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr  
245 250 255  
Phe Phe Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu  
260 265 270  
Gln Cys Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser  
275 280 285  
Val Ser Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys  
290 295 300  
Ala Ile Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly  
305 310 315 320  
Leu Ile Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu  
325 330 335

Leu Asp Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln  
                   340                  345                  350  
 Lys Cys Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu  
                   355                  360                  365  
 His Thr Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln  
                   370                  375                  380  
 Gln Tyr Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr  
                   385                  390                  395                  400  
 Ala Tyr Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu  
                   405                  410                  415  
 Leu Ala Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Arg Arg Ser Asn  
                   420                  425                  430  
 Ala Ser Tyr Ile Gln  
                   435

<210> 160  
 <211> 1134  
 <212> DNA  
 <213> H. sapiens

<400> 160  
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 cagcttcagt gctstcctct tcccgcgcgc tttgccccgc ccacatcact ttcgctccag 240  
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<210> 161  
 <211> 50  
 <212> PRT  
 <213> H. sapien

<220>  
 <221> misc\_feature  
 <222> (45)...(45)  
 <223> Xaa = Ile or Leu

<400> 161  
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 Ile Phe Asn Ser Ile Gln Val Val Pro Arg Ile His Glu Gly Asn Ile  
                   20                  25                  30  
 Ser Lys Gln Asp Glu Thr Met Met Thr Asp Leu Ser Xaa Pro Ser Ser  
                   35                  40                  45  
 Asn Phe  
   50

<210> 162

<211> 49  
 <212> PRT  
 <213> bovine  
  
 <220>  
 <221> misc\_feature  
 <222> (44)...(44)  
 <223> Xaa = Ile or Leu  
  
 <400> 162  
 Phe Gly Trp Val Thr Glu Leu Ala Ser Gln Thr Pro Gly Ser Glu Asn  
 1 5 10 15  
 Ile Phe Ser Phe Ile Lys Val Val Pro Gly Val His Glu Gly Asn Phe  
 20 25 30  
 Ser Lys Gln Asp Glu Lys Met Ile Asp Ile Ser Xaa Pro Ser Ser Asn  
 35 40 45  
 Phe  
  
 <210> 163  
 <211> 51  
 <212> PRT  
 <213> guinea pig  
  
 <220>  
 <221> misc\_feature  
 <222> (46)...(46)  
 <223> Xaa = Ile or Leu  
  
 <400> 163  
 Phe Gly Trp Val Leu Glu Leu Ala Tyr Gln Ser Pro Gly Ala Glu Asp  
 1 5 10 15  
 Ile Phe Asn Pro Val Lys Val Met Val Ala Leu Ser Ala His Glu Gly  
 20 25 30  
 Asn Ser Ser Asp Gln Asp Asp Thr Val Val Pro Ser Ser Xaa Pro Ser  
 35 40 45  
 Ser Asn Phe  
 50  
  
 <210> 164  
 <211> 49  
 <212> PRT  
 <213> rat  
  
 <220>  
 <221> misc\_feature  
 <222> (44)...(44)  
 <223> Xaa = Ile or Leu  
  
 <400> 164  
 Phe Gly Trp Val Ser Gln Leu Ala Ser His Asn Pro Val Thr Glu Asp  
 1 5 10 15  
 Ile Phe Asn Ser Thr Lys Ala Val Pro Lys Ile His Gly Gly Asp Ser  
 20 25 30  
 Ser Lys Gln Asp Glu Ile Met Val Asp Ser Ser Xaa Pro Ser Ser Asn  
 35 40 45  
 Phe  
  
 <210> 165  
 <211> 1767  
 <212> DNA  
 <213> Cavia sp.

<400> 165

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actgcaagga	ttaacagtga	gaacatgaag	ctgccacttt	tgatgtttcc	cgtgtgtctg	180
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aacgcgaaca	gtttttctga	ggctggggag	atagacgtag	atggagaggt	gaagatagct	300
ttgattggca	ttaaacagat	gaaaatcatg	atggaaagga	gagaggaaga	acacagcaaa	360
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gaagtccatg	aacacctgga	ggaggaagaa	agcttatgcc	aggtttctct	ggcagattcc	480
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gtatactaaa	taaatactga	gtcccct				1767